ABSTRACT OF THE DISCLOSURE

A BLAST analysis unit calculates the homologies between data included in an analysis target data group and the first data group, respectively, and calculates the number of data exhibiting homologies (orthologous gene count) as a first homology value $\underline{x}$ by using the calculated values. This unit sets n_A thresholds E and calculates a first homology value x_i for each threshold E_i, and calculates the homologies between data included in the analysis target data group and the second data group, respectively. The unit calculates the number of data exhibiting homologies (orthologous gene count) as a second homology value $\underline{y}$. The unit sets n_B thresholds E and calculates a second homology value y_i for each threshold E_i. A t-test unit determines to which one of the first and second data groups the analysis target data group is similar.